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AC U79117;
XX
SV U79117.1
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DT 04-SEP-1998 (Rel. 56, Created)
DT 04-SEP-1998 (Rel. 56, Last updated, Version 1)
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DE Clostridium thermocellum S-layer protein (slpA) gene, complete cds.
XX
KW .
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OS Clostridium thermocellum
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
XX
RN [1]
RP 1-3573
RX MEDLINE; 98129094.
RA Lemaire M., Miras I., Gounon P., Beguin P.;
RT "Identification of a region responsible for binding to the cell wall within
RT the S-layer protein of Clostridium thermocellum";
RL Microbiology 144 (Pt):0-0 (0).
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RN [2]
RP 1-3573
RA Miras I., Beguin P.;
RT ;
RL Submitted (20-NOV-1996) to the EMBL/GenBank/DDBJ databases.
RL Biotechnology, Institut Pasteur, 28, rue du Dr. Roux, Paris 75724 Cedex 15,
RL France
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DR SPTREMBL; 086999; 086999.
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[\[Keywords\]](#)
[\[Features\]](#)
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[\[Tools\]](#)

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Entry information

Entry name	O86999
Primary accession number	O86999
Secondary accession numbers	None
Entered in TrEMBL in	Release 08, November 1998
Sequence was last modified in	Release 08, November 1998
Annotations were last modified in	Release 24, June 2003

Name and origin of the protein

Protein name	S-layer protein
Synonyms	None
Gene name	SLPA
From	Clostridium thermocellum [TaxID: 1515]
Taxonomy	Bacteria ; Firmicutes ; Clostridia ; Clostridiales ; Clostridiaceae ; Clostridium .

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=NCIB 10682;

MEDLINE=98129094; PubMed=9467913; [NCBI, ExPASy, EBI, Israel, Japan]

Lemaire M., Miras I., Gounon P., Beguin P.:

"Identification of a region responsible for binding to the cell wall within the S-layer protein of Clostridium thermocellum.";

Microbiology 144:0-0(0).

Comments

None

Cross-references

EMBL	U79117; AAC33404.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence]
PIR	T30311; T30311.
InterPro	IPR001119 ; SLH. Graphical view of domain structure .
Pfam	PF00395 ; SLH; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	O86999 .
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SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

None

Features

None

Sequence information

Length: 1036 AA	Molecular weight: 113330 Da	CRC64: 1AF2202060D7C2A1 [This is a checksum on the sequence]
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O86999 in
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[PeptideMass](#), [PeptideCutter](#),
[Dotlet \(Java\)](#)



[ScanProsite](#),
[MotifScan](#)



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DT 03-DEC-2000 (Rel. 66, Created)
DT 10-APR-2001 (Rel. 67, Last updated, Version 3)
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RN [1]
RP 1-2434
RX MEDLINE; 21189268.
RX PUBMED; 11292772.
RA Karjalainen T.K., Waligora-Dupriet A.J., Cerquetti M., Spigaglia P.,
RA Mauri P., Mastrantonio P.;
RT "Molecular and genomic analysis of two genes encoding surface-anchored
RT proteins from Clostridium difficile";
RL Infect. Immun. 69(5):3442-3446 (2001).
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RN [2]
RP 1-2434
RA Karjalainen T.K.;
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RL Submitted (05-JUL-2000) to the EMBL/GenBank/DDBJ databases.
RL Microbiology, Univ Paris-Sud, Faculty of Pharmacy, 5, rue JB Clement,
RL Chatenay-Malabry 92296, France
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11

WEST Search History

DATE: Tuesday, August 12, 2003

Set Name Query

side by side

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 or therapeut\$).clm.

Hit Count Set Name

result set

17 L1

END OF SEARCH HISTORY

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L1: Entry 15 of 17

File: USPT

Nov 14, 1995

DOCUMENT-IDENTIFIER: US 5466672 A

TITLE: Therapeutic use of clostridium difficile toxin A

CLAIMS:

5. A method of treating cancer, comprising:

- a) providing i) a patient with gastrointestinal cancer, and ii) a preparation comprising *Clostridium difficile* toxin A in an aqueous solution in therapeutic amounts that is intravenously injectable; and
- b) intravenously injecting said toxin into said patient.

WEST

Generate Collection

Print

L1: Entry 9 of 17

File: USPT

Jun 27, 2000

DOCUMENT-IDENTIFIER: US 6080725 A

TITLE: Immunostimulating and vaccine compositions employing saponin analog adjuvants and uses thereof

CLAIMS:

12. The vaccine of claim 11, wherein said bacterial antigens are antigens associated with a bacterium selected from the group consisting of *Helicobacter pylori*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Ureaplasma urealyticum*, *Mycoplasma pneumoniae*, *Staphylococcus* spp., *Staphylococcus aureus*, *Streptococcus* spp., *Streptococcus pyogenes*, *Streptococcus pneumoniae*, *Streptococcus viridans*, *Enterococcus faecalis*, *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Bacillus anthracis*, *Salmonella* spp., *Salmonella typhi*, *Vibrio cholera*, *Pasteurella pestis*, *Pseudomonas aeruginosa*, *Campylobacter* spp., *Campylobacter jejuni*, *Clostridium* spp., *Clostridium difficile*, *Mycobacterium* spp., *Mycobacterium tuberculosis*, *Treponema* spp., *Borrelia* spp., *Borrelia burgdorferi*, *Leptospira* spp., *Hemophilus ducreyi*, *Corynebacterium diphtheriae*, *Bordetella pertussis*, *Bordetella parapertussis*, *Bordetella bronchiseptica*, *hemophilus influenza*, *Escherichia coli*, *Shigella* spp., *Erlichia* spp., *Rickettsia* spp. and combinations thereof.

WEST



Generate Collection

Print

L1: Entry 7 of 17

File: USPT

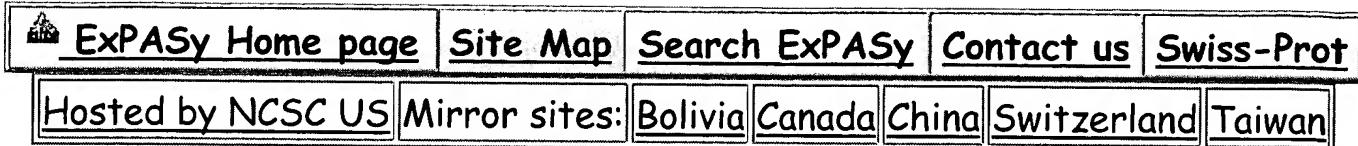
Jul 17, 2001

DOCUMENT-IDENTIFIER: US 6262029 B1

TITLE: Chemically modified saponins and the use thereof as adjuvants

CLAIMS:

29. The vaccine of claim 28, wherein said bacterial antigens are antigens associated with a bacterium selected from the group consisting of *Helicobacter pylori*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Ureaplasma urealyticum*, *Mycoplasma pneumoniae*, *Staphylococcus* spp., *Staphylococcus aureus*, *Streptococcus* spp., *Streptococcus pyogenes*, *Streptococcus pneumoniae*, *Streptococcus viridans*, *Enterococcus faecalis*, *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Bacillus anthracis*, *Salmonella* spp., *Salmonella typhi*, *Vibrio cholera*, *Pasteurella pestis*, *Pseudomonas aeruginosa*, *Campylobacter* spp., *Campylobacter jejuni*, *Clostridium* spp., *Clostridium difficile*, *Mycobacterium* spp., *Mycobacterium tuberculosis*, *Treponema* spp., *Borrelia* spp., *Borrelia burgdorferi*, *Leptospira* spp., *Hemophilus ducreyi*, *Corynebacterium diphtheriae*, *Bordetella pertussis*, *Bordetella parapertussis*, *Bordetella bronchiseptica*, *hemophilus influenza*, *Escherichia coli*, *Shigella* spp., *Erlichia* spp., *Rickettsia* spp. and combinations thereof.



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Entry information

Entry name	Q8KHB6
Primary accession number	Q8KHB6
Secondary accession numbers	None
Entered in TrEMBL in	Release 22, October 2002
Sequence was last modified in	Release 22, October 2002
Annotations were last modified in	Release 22, October 2002
Name and origin of the protein	
Protein name	S-layer protein variable domain SlpA [Fragment]
Synonyms	None
Gene name	SLPA
From	<u>Clostridium difficile</u> [TaxID: <u>1496</u>]
Taxonomy	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=ATCC 43597, 90-111, and 93-136;
MEDLINE=22083941; **PubMed**=12089261; [NCBI, ExPASy, EBI, Israel, Japan]
Karjalainen T., Saumier N., Barc M.C., Delmee M., Collignon A.:
"Clostridium difficile Genotyping Based on slpA Variable Region in S-Layer Gene Sequence: an Alternative to Serotyping.";
J. Clin. Microbiol. 40:2452-2458(2002).

Comments

None

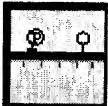
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	AF458882; AAM75946.1; -.	[EMBL / GenBank / DDBJ] [CodingSequence]
HOBACGEN	[Family / Alignment / Tree]	
ProtoMap	<u>Q8KHB6</u> .	
PRESAGE	<u>Q8KHB6</u> .	
ModBase	<u>Q8KHB6</u> .	
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Keywords

None

Features

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NON_TER	389	389		

Sequence information

Length: 389 AA [This is the length of the partial sequence]	Molecular weight: 41788 Da [This is the MW of the partial sequence]	CRC64: C5ED8F4901C18F8C [This is a checksum on the sequence]
--	--	---

10	20	30	40	50	60
AAPVFAATT	SEDNAGKYTV	VKDKYKDIFD	EVKKLVKEND	AAIDAYLKEN	NSTDRAAWT
70	80	90	100	110	120
ALAGTNSLNI	INITVKDSDD	DSVVVPKTVV	KTNTVVVDTDY	VENKLKNLDT	DEYVDFDITT
130	140	150	160	170	180
KASTVSSTKY	TAANIYDLAA	NNGKIIIDAL	KNVTEKQLKD	GGILGEVAKT	ISGATTPSAP
190	200	210	220	230	240
TGDTFASYFT	VGTVKTVNGK	VALEINIAEP	ASTVLVKTDA	ELTTSPQQ	KMSFANAKIT
250	260	270	280	290	300
LTEGDDRLLDF	SKPSIVDGAL	GDFAKAAATT	TPGKQQTINV	RVINAKQETV	KATDYDALKA
310	320	330	340	350	360
VVSKYKFDST	EIGRVYDEAK	DLNDKDKLDG	SSYDKDGTYK	AVFFAEGKRL	QGFSSYKGFS
370	380				
TDEAESGLAD	GNAALKLVIE	STDEDDFID			

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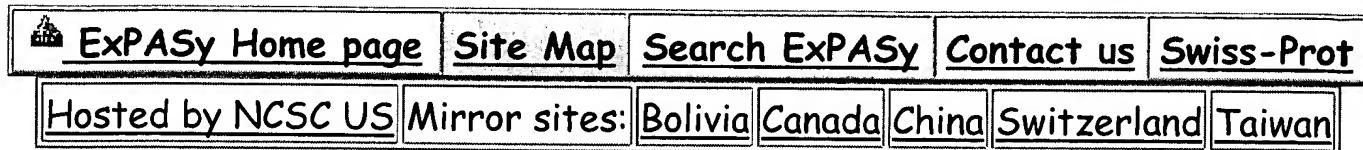
Sequence analysis tools: [ProtParam](#),
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[\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

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Entry information

Entry name	Q8KHH9
Primary accession number	Q8KHH9
Secondary accession numbers	None
Entered in TrEMBL in	Release 22, October 2002
Sequence was last modified in	Release 22, October 2002
Annotations were last modified in	Release 22, October 2002
Name and origin of the protein	
Protein name	S-layer protein variable domain SlpA [Fragment]
Synonyms	None
Gene name	SLPA
From	<u>Clostridium difficile</u> [TaxID: <u>1496</u>]
Taxonomy	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=56026, 54823, and ATCC 43601;
MEDLINE=22083941; **PubMed**=12089261; [NCBI, ExPASy, EBI, Israel, Japan]
Karjalainen T., Saumier N., Barc M.C., Delmee M., Collignon A.:
"Clostridium difficile Genotyping Based on slpA Variable Region in S-Layer Gene Sequence: an Alternative to Serotyping.";
J. Clin. Microbiol. 40:2452-2458(2002).

Comments

None

Cross-references

EMBL	AF458884; AAM75939.1; -.	[EMBL / GenBank / DDBJ] [CodingSequence]
	AF458885; AAM75940.1; -.	[EMBL / GenBank / DDBJ] [CodingSequence]
	AF458883; AAM75947.1; -.	[EMBL / GenBank / DDBJ] [CodingSequence]
HOBACGEN	[Family / Alignment / Tree]	
ProtoMap	<u>Q8KHH9</u>	
PRESAGE	<u>Q8KHH9</u>	
ModBase	<u>Q8KHH9</u>	
SWISS-2DPAGE	Get region on 2D PAGE.	

Keywords

None

Features

 Feature table viewer				
Key	From	To	Length	Description
NON_TER	1	1		
NON_TER	339	339		

Sequence information

Length: 339 AA [This is the length of the partial sequence]	Molecular weight: 36205 Da [This is the MW of the partial sequence]	CRC64: 9FDB0B05COFFAA61 [This is a checksum on the sequence]
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10	20	30	40	50	60
AAPVFANVVT	GSEGYTVSQQ	DYKKAVKQIQ	DGIKKNIITS	INIYFDGTVK	STVNVAGDQD
70	80	90	100	110	120
ARDKIADDNFN	NTVEGKLDSDL	GDGKYVDFEI	SYNKGVEEYT	KTELENYKKL	LDNKVVIPKA
130	140	150	160	170	180
SGVNPAGAVKE	KSGSADEAVA	ADNDIKGSQD	YNTTVEADTT	NGGYKLSITA	KTISDVKYGT
190	200	210	220	230	240
IGAGKYPDAK	VITATGTDAL	VKGKTVDISA	SYALEASTGN	VSGLSLTDTN	PSSDSVNVR
250	260	270	280	290	300
INAKEITIDL	DASSYDSAES	LAKKYVFKPS	TLTSIYTDIE	AGNIERVNGK	YQVEIFADGK
310	320	330			
RLNTLSAVNS	TIADPDSTAK	VIIKADKLKD	LKDYVDDLK		

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NiceProt View of TrEMBL: Q8KHI4

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[\[Features\]](#)
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Entry information

Entry name	Q8KHI4
Primary accession number	Q8KHI4
Secondary accession numbers	None
Entered in TrEMBL in	Release 22, October 2002
Sequence was last modified in	Release 22, October 2002
Annotations were last modified in	Release 22, October 2002

Name and origin of the protein

Protein name	S-layer protein [Fragment]
Synonyms	None
Gene name	SLPA
From	<u>Clostridium difficile</u> [TaxID: <u>1496</u>]
Taxonomy	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=ATCC 43598, GAI95600, and GAI95601;

MEDLINE=22083941; PubMed=12089261; [NCBI, ExPASy, EBI, Israel, Japan]

Karjalainen T., Saumier N., Barc M.C., Delmee M., Collignon A.:

"Clostridium difficile Genotyping Based on slpA Variable Region in S-Layer Gene Sequence: an Alternative to Serotyping.";

J. Clin. Microbiol. 40:2452-2458(2002).

Comments

None

Cross-references

EMBL	AF448125;	[EMBL / GenBank / DDBJ]
	AAM75925.1; -.	[CoDingSequence]
	AF448126;	[EMBL / GenBank / DDBJ]
	AAM75926.1; -.	[CoDingSequence]
	AF448127;	[EMBL / GenBank / DDBJ]
	AAM75927.1; -.	[CoDingSequence]
HOBACGEN	[Family / Alignment / Tree]	
ProtoMap	Q8KHI4.	
PRESAGE	Q8KHI4.	
ModBase	Q8KHI4.	
SWISS-2DPAGE	Get region on 2D PAGE.	

Keywords

None

Features

 Feature table viewer				
Key	From	To	Length	Description
NON_TER	1	1		
NON_TER	354	354		

Sequence information

Length: 354 AA [This is the length of the partial sequence]	Molecular weight: 37738 Da [This is the MW of the partial sequence]	CRC64: 9D558CDF0B136E10 [This is a checksum on the sequence]
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AAPIFADSTT	PGYTUVVKNDW	KKAVKQLQDG	LKNKTISTIK	VSFNGNSVGE	VTPASSGAKK	
70	80	90	100	110	120	
ADRDAAAEKL	YNLVNTQLDK	LGDGGDYVDFE	VTYNLATQII	TKAEEAEAVLT	KLQQYNDKVL	
130	140	150	160	170	180	
INSATDTVKG	MVSDTQVDSK	NVAANPLKVS	DMYTIPSAIT	GSDDSGYSIA	KPTEKTTSL	
190	200	210	220	230	240	
YGTVGDATA	G KAITVDTASN	EAFAGNGKVI	DYNKSFKATV	QGDGTVKTSG	VVLKDASDMA	
250	260	270	280	290	300	
ATGTIKVRVT	SAKEESIDVD	SSSYISAENL	AKKYVFNPKE	VSEAYNAIVA	LQNDGIESSDL	
310	320	330	340	350		
VQLVNGKYQV	I FYPEGKRLE	TKSADIJADA	DSPAKITIKA	NKLKDLKDYV	DDLK	

[Q8KHI4 in FASTA format](#)

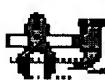
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